

L Number	Hits	Search Text	DB	Time stamp
1	1203	linear adj2 programming	USPAT; US-PGPUB	2003/05/21 12:28
2	9	(linear adj2 programming) and hybridiz\$6 and intensit\$4	USPAT; US-PGPUB	2003/05/21 12:24
3	16	(linear adj2 programming) and probe and hybridiz\$6	USPAT; US-PGPUB	2003/05/21 12:26
4	20	(linear adj2 programming) and hybridiz\$6	USPAT; US-PGPUB	2003/05/21 12:26
5	4	((linear adj2 programming) and hybridiz\$6) not ((linear adj2 programming) and probe and hybridiz\$6)	USPAT; US-PGPUB	2003/05/21 12:27
6	316	linear adj2 programming	EPO; JPO; DERWENT; IBM_TDB	2003/05/21 12:28
7	3	(linear adj2 programming) and (probe or oligonucleotide or hybridiz\$6 or intensit\$4)	EPO; JPO; DERWENT; IBM_TDB	2003/05/21 12:29
8	6	(linear adj2 programming) and (hybrid\$8 or intensit\$4)	EPO; JPO; DERWENT; IBM_TDB	2003/05/21 12:30
9	2	(linear adj2 programming) and (DNA or RNA or probe or nucleic or nucleotide or oligo\$ or primer)	EPO; JPO; DERWENT; IBM_TDB	2003/05/21 12:31
10	9	(linear adj2 programming) and (array or microarray)	EPO; JPO; DERWENT; IBM_TDB	2003/05/21 12:32

FD 12/21/00

minimizing?
effect of cross-hybridization
w/ linear programming
effect $\neq 0$

STN Columbus

10538.
 ISSN: 1066-5277.
 DT Article; Journal
 FS LIFE
 LA English
 REC Reference Count: 26
 ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS
 AB The problem addressed in this paper is concerned with DNA sequencing by **hybridization**. An algorithm is proposed that solves a computational phase of this approach in the presence of both positive and negative errors resulting from the **hybridization** experiment. No a priori knowledge of the nature and source of these errors is required. An extensive set of computational experiments showed that the algorithm behaves surprisingly well if only positive errors appear. The general case, where positive and negative errors occur, can be also solved satisfactorily for an error rate up to 10%.

L3 ANSWER 19 OF 19 CAPLUS COPYRIGHT 2003 ACS
Full Text
 AN 1997:738748 CAPLUS
 DN 128:57887
 TI A branch-and-cut approach to physical mapping of chromosomes by unique end-probes
 AU Christof, Thomas; Junger, Michael; Kececiloglu, John; Mutzel, Petra; Reinelt, Gerhard
 CS Institut fur Angewandte Mathematik, Universitat Heidelberg, Heidelberg, 69120, Germany
 SO Journal of Computational Biology (1997), 4(4), 433-447
 CODEN: JCOBEM; ISSN: 1066-5277
 PB Mary Ann Liebert, Inc.
 DT Journal
 LA English
 AB A fundamental problem in computational biol. is the construction of phys. maps of chromosomes from **hybridization** expts. between unique probes and clones of chromosome fragments in the presence of error. Alizadeh, Karp, Weissner and Zweig (Algorithmica 13:1/2, 52-76, 1995) first considered a max.-likelihood model of the problem that is equiv. to finding an ordering of the probes that minimizes a weighted sum of errors and developed several effective heuristics. The authors show that by exploiting information about the end-probes of clones, this model can be formulated as a Weighted Betweenness Problem. This affords the significant advantage of allowing the well-developed tools of integer **linear-programming** and branch-and-cut algorithms to be brought to bear on phys. mapping, enabling the authors for the first time to solve small mapping instances to optimality even in the presence of high error. The authors also show that by combining the optimal soln. of many small overlapping Betweenness Problems, one can effectively screen errors from larger instances and solve the edited instance to optimality as a Hamming-Distance Traveling Salesman Problem. This suggests a new approach, a Betweenness-Traveling Salesman hybrid, for constructing phys. maps.

=> d his

(FILE 'HOME' ENTERED AT 10:35:32 ON 21 MAY 2003)

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, AQUASCI, BIOBUSINESS, BIOCOMMERCE, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CANCERLIT, CAPLUS, CEABA-VTB, CEN, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DRUGB, DRUGLAUNCH, DRUGMONOG2, ...' ENTERED AT 10:35:51 ON 21 MAY 2003

SEA LINEAR (W) PROGRAM? AND (ARRAY OR NUCLEIC (W) ACID OR MICRO

STN Columbus

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2   FILE CAPLUS
1   FILE IFIPAT
1   FILE SCISEARCH
17  FILE USPATFULL
2   FILE USPAT2
L1  QUE LINEAR (W) PROGRAM? AND (ARRAY OR NUCLEIC (W) ACID OR MICRO
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FILE 'USPATFULL, CAPLUS, USPAT2, IFIPAT, SCISEARCH' ENTERED AT 10:39:21
ON 21 MAY 2003

L2 23 S L1
L3 19 DUP REM L2 (4 DUPLICATES REMOVED)

=> log y

COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	62.28	65.79
DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)	SINCE FILE ENTRY	TOTAL SESSION
CA SUBSCRIBER PRICE	-0.65	-0.65

STN INTERNATIONAL LOGOFF AT 10:44:24 ON 21 MAY 2003

STN Columbus

CS Heidelberg Univ. (Germany, F.R.). Interdisziplinäres Zentrum
Wissenschaftliches Rechnen. (012073029 9205001)
NR TIB/A97-01563/XAB; IWR--96-39(PREPR.)
21p; Aug 1996
DT Report
CY Germany, Federal Republic of
LA English
AV Order this product from NTIS by: phone at 1-800-553-NTIS (U.S.
customers); (703)605-6000 (other countries); fax at (703)605-6900; and
email at orders@ntis.gov. NTIS is located at 5285 Port Royal Road,
Springfield, VA, 22161, USA.
NTIS Prices: PC E09
OS GRA V9704
AB A fundamental problem in computational biology is the construction of
physical maps of chromosomes from **hybridization** experiments between
unique probes and clones of chromosome fragments in the presence of
error. Alizadeh, Karp, Weisser and Zweig AKWZ94 first considered a
maximum-likelihood model of the problem that is equivalent to finding an
ordering of the probes that minimizes a weighted sum of errors, and
developed several effective heuristics. We show that by exploiting
information about the end-probes of clones, this model can be formulated
as a weighted Betweenness Problem. This affords the significant
advantage of allowing the well-developed tools of integer
linear-programming and branch-and-cut algorithms to be brought to
bear on physical mapping, enabling us for the first time to solve small
mapping instances to optimality even in the presence of high error. We
also show that by combining the optimal solution of many small
overlapping Betweenness Problems, one can effectively screen errors from
larger instances, and solve the edited instance to optimality as a
Hamming-Distance Traveling Salesman Problem. This suggests a new
combined approach to physical map construction. (orig.). (Copyright (c)
1997 by FIZ. Citation no. 97:001563.)

=> d his

(FILE 'HOME' ENTERED AT 10:55:06 ON 21 MAY 2003)

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, AQUASCI,
BIOBUSINESS, BIOCOMMERCE, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA,
CANCERLIT, CAPLUS, CEABA-VTB, CEN, CIN, CONFSCI, CROPB, CROPU, DDFB,
DDFU, DGENE, DRUGB, DRUGLAUNCH, DRUGMONOG2, ...' ENTERED AT 10:55:19 ON
21 MAY 2003

SEA LINEAR (W) PROGRAM? AND HYBRIDIZ?

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2  FILE BIOSIS
2  FILE BIOTECHNO
2  FILE CAPLUS
2  FILE EMBASE
1  FILE ESBIODASE
1  FILE IFIPAT
7  FILE JICST-EPLUS
1  FILE LIFESCI
1  FILE MEDLINE
2  FILE NTIS
4  FILE PASCAL
6  FILE SCISEARCH
21 FILE USPATFULL
2  FILE USPAT2

```

L1 QUE LINEAR (W) PROGRAM? AND HYBRIDIZ?

STN Columbus

FILE 'JICST-EPLUS, SCISEARCH, PASCAL, BIOSIS, BIOTECHNO, CAPLUS, EMBASE,
NTIS, USPAT2, ESBIODBASE, IFIPAT, LIFESCI, MEDLINE' ENTERED AT 10:56:43 ON
21 MAY 2003

L2 33 S L1
L3 22 DUP REM L2 (11 DUPLICATES REMOVED)
L4 22 FOCUS L3 1-

=> log y

COST IN U.S. DOLLARS	SINCE FILE	TOTAL
	ENTRY	SESSION
FULL ESTIMATED COST	74.18	75.49
DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)	SINCE FILE	TOTAL
	ENTRY	SESSION
CA SUBSCRIBER PRICE	-0.65	-0.65

STN INTERNATIONAL LOGOFF AT 10:57:45 ON 21 MAY 2003